

GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 25 Seconds  
(Without alignments)  
29.663 Million cell updates/sec

Title: US-10-006-190-1-copy\_6-23  
Perfect score: 88  
Sequence: 1 RLRAVINGAPGSGKGTV.18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	88	100.0	226	1 KAD3_HUMAN	Q9U1J7 homo sapien
2	84	95.5	226	1 KAD3_BOVIN	P08760 bos taurus
3	84	95.5	226	1 KAD3_RAT	P29411 ratius norv
4	77	87.5	223	1 KAD4_HUMAN	P27144 homo sapien
5	77	87.5	223	1 KAD4_MOUSE	Q6WU9 mus musculu
6	77	87.5	223	1 KAD4_RAT	Q6WU9 mus musculu
7	75	85.2	219	1 KAD3_MOUSE	Q6WU9 mus musculu
8	62	70.5	214	1 KAD_MYCGA	Q52357 mus musculu
9	62	70.5	225	1 KAD2_YEAST	P63664 saccharomyc
10	61	69.3	245	1 KAD_CHLTR	Q84110 chlamydia t
11	61	69.3	253	1 KAD_CHLMU	Q9PKT0 chlamydia m
12	60	68.2	215	1 KAD_PSEAE	Q9HXV4 pseudomonas
13	60	68.2	216	1 KAD_PSEPU	Q92409 pseudomonas
14	60	68.2	231	1 KAD2_MOUSE	Q6WU9 mus musculu
15	60	68.2	238	1 KAD2_HUMAN	P54819 homo sapien
16	60	68.2	238	1 KAD2_RAT	P29410 ratius norv
17	60	68.2	251	1 KADX_CAEEL	P24346 caenorhabdi
18	59	67.0	214	1 KAD_ECOLI	P05082 escherichia
19	59	67.0	214	1 KAD_SALTY	P37407 salmonella
20	59	67.0	214	1 KAD_VIBCH	Q9K1B7 vibrio chol
21	59	67.0	214	1 KAD_YEREN	P34312 yersinia en
22	59	67.0	214	1 KAD_YERPE	O69172 yersinia pe
23	59	67.0	215	1 KAD_BUCAL	P37556 buchneria ap
24	59	67.0	215	1 KAD_NEICO	P49979 neisseria g
25	59	67.0	215	1 KAD_NEIMA	P49980 neisseria m
26	59	67.0	222	1 KAD_FALSO	Q8XWE1 ralsconia s
27	59	67.0	240	1 KAD2_BOVIN	P08166 bos taurus
28	59	67.0	248	1 KAD_GIALA	P49982 giardia lam
29	58	65.9	187	1 KAD_XYLRA	O69PM3 xyliella fas
30	58	65.9	443	1 ERAL_HUMAN	O75616 homo sapien
31	57	64.8	203	1 KAD_MICLU	P33107 micrococcus
32	56	63.6	181	1 KAD_MYCLE	O33007 mycobacteri
33	56	63.6	213	1 KAD_CHLPN	Q9Z8U0 chlamydia p

34	56	63.6	214	1 KAD_HAEIN	P24323 haemophilus
35	56	63.6	214	1 KAD_PASMU	P57837 pasteurella
36	55	62.5	181	1 KAD_CORGL	P49973 corynebacte
37	55	62.5	215	1 KAD_LISTIN	O927M8 listeria in
38	55	62.5	215	1 KAD_LISTMO	O8Y49 listeria mo
39	55	62.5	215	1 KAD_NEIMU	P49981 neisseria m
40	54	61.4	36	1 KAD_STRGR	P33398 streptomyce
41	54	61.4	70	1 KAD_STRSC	P43417 streptomyce
42	54	61.4	176	1 AROK_MYCTU	P95014 mycobacteri
43	54	61.4	185	1 KAD1_SYMK3	P73302 synechocyst
44	54	61.4	194	1 KAD1_BROME	O8YH19 druceella me
45	54	61.4	198	1 KAD_RHILO	O98N36 rhizobium 1

## ALIGNMENTS

RESULT 1									
KAD3_HUMAN	STANDARD;	PRT;	226 AA.						
ID	KAD3_HUMAN								
AC	Q9U1J7;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	GRP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3) (AK3-alpha).								
DE	AK3.								
GN	Homo sapiens (Human).								
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Liver;								
RA	Noma T.;								
RL	Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.								
CC	-1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.								
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).								
CC	-1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).								
CC	-1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.								
CC	-----								
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CC	-----								
DR	EMBL; AB021870; BAA87913.1; -								
DR	HSSP; P08760; 2AK3.								
DR	InterPro; IPR000850; Adenylate_kin.								
DR	Pfam; PF00406; adenylatekinase; 1.								
DR	PRINTS; PR00094; ADENYLTKINASE.								
DR	ProDom; PD000657; Adenylate_kin; 1.								
DR	PROSITE; PS00113; ADENYLATE_KINASE; 1.								
KW	Transferase; Kinase; GTP-binding; Mitochondrion.								
FT	NP-BIND 0								
FT	INT_MET 0								
FT	NP-BIND 13								
FT	INT_MET 21								
SQ	SEQUENCE 226 AA; 25507 MW; 9F623E32A95B20C3 CRC64;								
Query Match									
Best Local Similarity 100.0%; Score 88; DB 1; Length 226;									
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	1 RLRAVINGAPGSGKGTV 18								
DB	5 RLRAVINGAPGSGKGTV 22								
RESULT 2									
KAD3_BOVIN	STANDARD;	PRT;	226 AA.						
ID	KAD3_BOVIN								

AC P08760;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).  
 GN AK3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90037053; PubMed=2478555;  
 RA Yamada M., Shahjahan M., Tanabe T., Kishi F., Nakazawa A.;  
 RT "Cloning and characterization of cDNA for mitochondrial GTP:AMP  
 RT phosphotransferase of bovine liver.";  
 RT J. Biol. Chem. 264:19192-19199(1989).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE-Heart;  
 RX MEDLINE=86248102; PubMed=3013690;  
 RA Tomasselli A.G., Frank R., Schiltz E.;  
 RT "The complete primary structure of GTP:AMP phosphotransferase from  
 RT beef heart mitochondria.";  
 RT FEBS Lett. 202:303-308(1986).  
 RN [3]  
 RP SEQUENCE OF 1-49 FROM N.A.  
 RX MEDLINE=92084124; PubMed=1748300;  
 RA Shahjahan M., Yamada M., Tanaka H., Nakazawa A.;  
 RT "Cloning and characterization of the gene encoding bovine  
 RT mitochondrial adenylate kinase isozyme 3.";  
 RT Gene 107:313-317(1991).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=91084487; PubMed=2175649;  
 RA Diederichs K., Schulz G.E.;  
 RT "Three-dimensional structure of the complex between the mitochondrial  
 RT matrix adenylate kinase and its substrate AMP.";  
 RL Biochemistry 29:8138-8144(1990).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).  
 RX MEDLINE=91132661; PubMed=1994037;  
 RA Diederichs K., Schulz G.E.;  
 RT "The refined structure of the complex between adenylate kinase from  
 RT beef heart mitochondria and its substrate AMP at 1.85-A  
 RT resolution.";  
 RL J. Mol. Biol. 217:541-549(1991).  
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: D10376; BAA01210.1;  
 DR EMBL: D10373; BAA01210.1; JOINED.  
 DR EMBL: D10374; BAA01210.1; JOINED.  
 DR EMBL: D10375; BAA01210.1; JOINED.  
 DR EMBL: M25757; AAA30705.1;  
 DR PIR: A24201; A24201.  
 DR PIR: A34442; A34442.  
 DR PIR: JH0512; JH0512.  
 DR PDB: 2AK3; 12-MAY-95.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.

DR Prodom; PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE KINASE; 1.  
 KW Transferase; Kinase; GTP-binding; Mitochondrion; 3D-structure.  
 FT INIT\_MET 0  
 FT NP\_BIND 13 21  
 FT STRAND 10 10  
 FT STRAND 8 12  
 FT TURN 15 16  
 FT HELIX 19 29  
 FT STRAND 33 36  
 FT HELIX 37 45  
 FT TURN 46 48  
 FT HELIX 50 60  
 FT TURN 61 62  
 FT HELIX 67 79  
 FT TURN 80 81  
 FT STRAND 86 89  
 FT HELIX 95 102  
 FT TURN 103 104  
 FT STRAND 109 114  
 FT HELIX 117 124  
 FT TURN 125 125  
 FT STRAND 127 130  
 FT TURN 131 134  
 FT STRAND 135 138  
 FT TURN 139 141  
 FT STRAND 142 142  
 FT TURN 147 148  
 FT STRAND 149 149  
 FT TURN 151 153  
 FT STRAND 156 156  
 FT STRAND 158 158  
 FT TURN 161 162  
 FT HELIX 165 189  
 FT TURN 190 190  
 FT STRAND 192 196  
 FT HELIX 200 212  
 FT TURN 213 214  
 SQ SEQUENCE 226 AA; 25540 MW; 2B74C2FBA0A7CBA9 CRC64;  
 Query Match 95.5%; Score 84; DB 1; Length 226;  
 Best Local Similarity 94.4%; Pred. No. 3.5e-05;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RLRAVIMGAPSGSGKTV 18  
 DB 5 RLRAVIMGAPSGSGKTV 22  
 KAD3\_RAT  
 ID KAD3\_RAT STANDARD; PRT; 226 AA.  
 AC P29411;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).  
 GN AK3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93224500; PubMed=8468325;  
 RA Tanabe T., Yamada M., Noma T., Kajii T., Nakazawa A.;  
 RT "Tissue-specific and developmentally regulated expression of the  
 RT gene encoding adenylate kinase isozymes.";  
 RL J. Biochem. 113:200-207(1993).  
 CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC -----
DR EMBL: D13062; BAA02379.1; -
DR PIR: J01945; J01945.
DR HSSP: P08760; 2AK3.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin. 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; GTP-binding; Mitochondrion.
DR INIT_MET 0 BY SIMILARITY.
DR NP_BIND 13 21 GTP (BY SIMILARITY).
DR SEQUENCE 226 AA; 25307 MW; D57FF37404AA6625 CRC64;

Query Match 95.5%; Score 84; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGSGKT 17
Db 5 RLRAVINGAPSGSGKT 21

RESULT 4
KADA_HUMAN
ID KADA_HUMAN STANDARD: PRT; 223 AA.
AC P27144;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK4 OR AK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92347846; PubMed=1639383;
RX Xu G., O'Connell P., Stevens J., White R.;
RT "Characterization of human adenylate kinase 3 (AK3) cDNA and mapping
RT of the AK3 pseudogene to an intron of the NFI gene.";
RL Genomics 13:537-542(1992).
RN
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC -----
DR EMBL: X60673; CAA43088.1; -
DR EMBL: BC016180; AAH16180.1; -
DR PIR: S16381; S16381.

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DR PIR: S16380; S16380.
DR PIR: A42820; A42820.
DR HSSP: P08760; 2AK3.
DR Genew; HGNC:363; AK3.
DR MIM: 103030; -
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin. 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
DR Transferrase; Kinase; GTP-binding; Mitochondrion.
DR INIT_MET 12 20 GTP (BY SIMILARITY).
DR NP_BIND 12 20 GTP (BY SIMILARITY).
DR SEQUENCE 223 AA; 25268 MW; 653341A8B3BC723 CRC64;

Query Match 87.5%; Score 77; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 0.00035;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RLRAVINGAPSGSGKT 18
Db 4 RLRAVINGAPSGSGKT 21

RESULT 5
KADA_MOUSE
ID KADA_MOUSE STANDARD: PRT; 223 AA.
AC Q9WUR9; Q9WUR9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK4 OR AK-4 OR AK3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC MEDLINE=99033072; PubMed=9813319;
RX Yoneda T., Sato M., Maeda M., Takagi H.;
RA "Identification of a novel adenylate kinase system in the brain:
RT cloning of the fourth adenylate kinase ";
RL Brain Res. Mol. Brain Res. 62:187-195(1998).
RN
RN SEQUENCE FROM N.A.
RA Noma T.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE
CC HIPPOCAMPUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
CC REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
CC THE ADULTHOOD IN THE RODENT.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC -----
DR EMBL: D85036; BAA77760.1; -
DR EMBL: AB020239; BAA77363.1; -
DR HSSP: P08760; 2AK3.
DR MGD: MGI:67980; AK4.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase. 1.
DR PRINTS: PR00094; ADENYLTKINASE.

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DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KM Transferase; Kinase; GTP-binding; Mitochondrion.  
 FT NP\_BIND 12 20 GTP (BY SIMILARITY).  
 FT CONFLICT 68 68 V -> A (IN REF. 2).  
 FT CONFLICT 187 187 S -> N (IN REF. 2).  
 FT CONFLICT 190 190 V -> M (IN REF. 2).  
 SQ SEQUENCE 223 AA; 25061 MW; 50552294971515EC CRC64;

Query Match 87.5%; Score 77; DB 1; Length 223;  
 Best Local Similarity 83.3%; Pred. No. 0.00035;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKGV 18  
 :|||||:|||||  
 Db 4 KLRRAVILGPPGSGKGV 21

RESULT 6  
 KAD4\_RAT ID KAD4\_RAT STANDARD; PRT; 223 AA.

AC O9WUS0;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP  
 transphosphorylase).  
 GN AK4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RP SEQUENCE FROM N.A.

RC STRAIN=Histar; TISSUE=Forebrain;  
 RX MEDLINE=99033072; PubMed=9813319;

RA Yoneda T., Sato M., Maeda M., Takagi H.;  
 RT "Identification of a novel adenylate kinase system in the brain:  
 cloning of the fourth adenylate kinase.";  
 RL Brain Res. Mol. Brain Res. 62:187-195(1998).

CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (potential).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PIRAMIDAL CELLS IN THE  
 HIPPOCAMPUS.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A  
 REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO  
 THE ADULTHOOD IN THE RODENT.

CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 -----

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CC EMBL: D87809; BAA77761.1; -  
 DR HSSP: P08760; ZAK3.  
 DR InterPro: IPR000850; Adenylate\_kin.

DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.

DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KM Transferase; Kinase; GTP-binding; Mitochondrion.  
 FT NP\_BIND 12 20 GTP (BY SIMILARITY).

FT SEQUENCE 223 AA; 25203 MW; B5A9BE45CF3C19B CRC64;  
 SQ

Query Match 87.5%; Score 77; DB 1; Length 223;  
 Best Local Similarity 83.3%; Pred. No. 0.00035;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKGV 18

Db :|||||:|||||  
 4 KLRRAVILGPPGSGKGV 21

RESULT 7  
 KAD3\_MOUSE ID KAD3\_MOUSE STANDARD; PRT; 219 AA.

AC O9WTP7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3)  
 DE (Fragment).  
 GN AK3 OR AK-3.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.

RA Noma T.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).

CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 -----

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CC EMBL: AB020203; BAA77360.1; -  
 DR HSSP: P08760; ZAK3.  
 DR MGD: MGI:87979; AK3.

DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.

DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.

DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KM Transferase; Kinase; GTP-binding; Mitochondrion.  
 FT NP\_BIND 1 14 GTP (BY SIMILARITY).

FT SEQUENCE 219 AA; 24640 MW; 7DDB8DF2C0BE7C5 CRC64;  
 SQ

Query Match 85.2%; Score 75; DB 1; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RAVIMGAPGSGKGV 18  
 :|||||:|||||  
 Db 1 RAVIMGAPGSGKGV 15

RESULT 8  
 KAD\_MYCGA ID KAD\_MYCGA STANDARD; PRT; 214 AA.

AC O52352;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
 GN ADK.

OS Mycoplasma gallisepticum.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI\_TaxID=2096;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=A5969Var.B;

RA Skamrov A., Feoktistova E., Goldman M., Beabealashvili R.;

RA Mosedale D., Nakahara K., Namath A., Norngren R., Oefner P., Oh C.,  
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,  
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;  
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: THIS SMALL UBICUOUS ENZYME IS ESSENTIAL FOR  
CC MAINTENANCE AND CELL GROWTH.  
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
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CC -----  
CC EMBL: M77757; AAA34418.1; -;  
CC EMBL: X65126; CAA6254.1; -;  
CC EMBL: U18922; AAB64697.1; -;  
CC PIR: JCI135; JCI135.  
CC PIR: S23568; S23568.  
CC HSSP: P08760; 2AK3.  
CC SGD: S0000972; ADK2.  
CC InterPro: IPR000850; Adenylate\_kin.  
CC Pfam: PF00406; adenylatekinase\_1.  
CC PRINTS: PR00094; ADENYLTKINASE.  
CC ProDom: PD000657; Adenylate\_kin; 1.  
CC PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
KW Transferase; kinase; ATP-binding; Mitochondrion.  
FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
SQ SEQUENCE 225 AA; 25194 MW; 36192BE2355BF91F CRC64;  
  
Query March 70.5%; Score 62; DB 1; Length 225;  
Best Local Similarity 73.3%; Pred. No. 0.049;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 LRAVINGAPGSGSGKT 17  
||:::|||||||  
Db 15 LRLLLGAPGSGGKT 29  
  
RESULT 10  
KAD\_CHLTR STANDARD; PRT; 245 AA.  
ID KAD\_CHLTR 14  
AC 064130;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
GN AKK OR Cn128.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D/UM-3/Cx;  
RX MEDLINE=99000809; PubMed=9784136.  
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
RA Mitchell W.P., Olinger L., Tatunov R.L., Zhao Q., Koonin E.V.,  
RA Davis R.W.;  
RT "Genome sequence of an obligate intracellular pathogen of humans:  
RT Chlamydia trachomatis";  
RL Science 282:754-759(1998).  
CC -1- FUNCTION: THIS SMALL UBICUOUS ENZYME IS ESSENTIAL FOR  
CC MAINTENANCE AND CELL GROWTH.  
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
CC -----  
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 CC -----  
 DR EMBL: AE001286; AAC67719.1; -  
 DR HSSP: P08760; 2AK3.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW Transferase; Kinase; ATP-binding; Complete proteome.  
 FT NP BIND 12 ATP (BY SIMILARITY).  
 SQ SEQUENCE 245 AA; 27784 MM; 3F38D306ED75D09F CRC64;  
 Query Match 69.3%; Score 61; DB 1; Length 245;  
 Best Local Similarity 91.7%; Pred. No. 0.074;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VINGAPSGSGKT 17  
 Db 9 IIMGAPSGSGKT 20  
 RESULT 11  
 KAD\_CHLMU STANDARD; PRT; 253 AA.  
 ID KAD\_CHLMU  
 AC Q9PKR0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
 GN ADK OR TC0404.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOPN / Nig9;  
 RA MEDLINE=20150235; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gall S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utecherback T., Berry K., Baas S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwyn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE002307; AAF39261.1; -  
 DR HSSP: P08760; 2AK3.  
 DR TIGR: TC0404; -  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 FT NP BIND 12 ATP (BY SIMILARITY).  
 SQ SEQUENCE 245 AA; 27784 MM; 3F38D306ED75D09F CRC64;

DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW Transferase; Kinase; ATP-binding; Complete proteome.  
 FT NP BIND 12 ATP (BY SIMILARITY).  
 SQ SEQUENCE 253 AA; 28597 MM; 9F915F6ECBBAFDD CRC64;  
 Query Match 69.3%; Score 61; DB 1; Length 253;  
 Best Local Similarity 91.7%; Pred. No. 0.076;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VINGAPSGSGKT 17  
 Db 9 IIMGAPSGSGKT 20  
 RESULT 12  
 KAD\_PSEAE STANDARD; PRT; 215 AA.  
 ID KAD\_PSEAE  
 AC Q9HXV4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).  
 GN ADK OR PA3686.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OX Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RA MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olsen M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE004788; AAC07074.1; -  
 DR HSSP: P05082; 1E4V.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW Transferase; Kinase; ATP-binding; Complete proteome.  
 FT NP BIND 7 ATP (BY SIMILARITY).  
 SQ SEQUENCE 215 AA; 23107 MM; 744C9FDC51EC057 CRC64;  
 Query Match 68.2%; Score 60; DB 1; Length 215;  
 Best Local Similarity 60.0%; Pred. No. 0.09;  
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 LRAVIMGAPSGSGKT 17  
 Db 1 MRVILLGAPGAGKT 15

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RESULT 13
KAD_PSEPU          STANDARD;          PRT;          216 AA.
ID   KAD_PSEPU
AC   Q92409;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN   ADK.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mt-2;
RA   Takeoka H., Miura K., Nakazawa A.;
RT   "Complete adk gene from Pseudomonas putida mt-2."
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDI databases.
CC   -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC       MAINTENANCE AND CELL GROWTH.
CC   -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC   -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC   -----
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CC   -----
DR   EMBL: AB024426; BAA75818.1; -
DR   HSSP: P05082; 1E4V.
DR   InterPro: IPR000850; Adenylate_kin.
DR   Pfam: PF00406; adenylatekinase; 1.
DR   PRINTS: PR00094; ADENYLTKINASE.
DR   ProDom: PD000657; Adenylate_kin; 1.
DR   PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW   Transferase; Kinase; ATP-binding.
FT   NP_BIND 7 15
SQ   SEQUENCE 216 AA; 23222 MW; C7EC04EC62C9ECA7 CRC64;

Query Match          68.2%; Score 60; DB 1; Length 216;
Best Local Similarity 60.0%; Pred. No. 0.09;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY   3 LRAVINGAPGSGKGT 17
DB   1 MRVILGAPGAGKGT 15

RESULT 14
KAD2_MOUSE
ID   KAD2_MOUSE          STANDARD;          PRT;          231 AA.
AC   Q9WTP6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE   transphosphorylase).
GN   AK2 OR AK-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Noma T.;

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RL   Submitted (NOV-1998) to the EMBL/GenBank/DDI databases.
CC   -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC       MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
CC   -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC   -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space (By
CC       similarity).
CC   -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC   -----
DR   EMBL: AB020202; BAA77359.1; -
DR   HSSP: P08166; 1AK2.
DR   MGD: MGI:87978; AK2.
DR   InterPro: IPR000850; Adenylate_kin.
DR   Pfam: PF00406; adenylatekinase; 1.
DR   PRINTS: PR00094; ADENYLTKINASE.
DR   ProDom: PD000657; Adenylate_kin; 1.
DR   PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW   Transferase; Kinase; ATP-binding; Mitochondrion.
FT   INIT_MET 0
FT   NP_BIND 21 29
SQ   SEQUENCE 231 AA; 25693 MW; A90DA6797CFE5E1E CRC64;

Query Match          68.2%; Score 60; DB 1; Length 231;
Best Local Similarity 66.7%; Pred. No. 0.097;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY   3 LRAVINGAPGSGKGT 17
DB   15 ITRVILGPPGAGKGT 29

RESULT 15
KAD2_HUMAN
ID   KAD2_HUMAN          STANDARD;          PRT;          238 AA.
AC   P54819; O16856;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE   transphosphorylase).
GN   AK2 OR ADK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   MEDLINE=97000211; PubMed=8843353;
RA   Lee Y., Kim J.W., Lee I.A., Kang H.B., Choe Y.K., Lee H.G.,
RA   Lim J.S., Kim H.J., Park C., Choe I.S.;
RT   "Cloning and characterization of cDNA for human adenylate kinase 2A."
RL   Biochem. Mol. Biol. Int. 39:833-842(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   MEDLINE=98162934; PubMed=9504408;
RA   Lee Y., Kim J.W., Lee S.M., Kim H.J., Lee K.S., Park C., Choe I.S.;
RT   "Cloning and expression of human adenylate kinase 2 isozyms:
RT   differential expression of adenylate kinase 1 and 2 in human muscle
RT   tissues."
RL   J. Biochem. 123:47-54(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RA   Strausberg R.;

```





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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 43 Seconds  
(without alignments)  
40.242 Million cell updates/sec

Title: US-10-006-190-1\_COPY\_6\_23

Perfect score: 88

Sequence: 1 RLRRAVIMGAPSGSGKTIV 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	95.5	227	2 J01945	nucleoside-triphos
2	84	95.5	227	2 A34442	nucleoside-triphos
3	77	87.5	223	1 K1H0A3	nucleoside-triphos
4	62	70.5	198	2 B82825	adenylate kinase x
5	62	70.5	225	2 S23568	adenylate kinase (
6	61	69.3	245	2 D71554	probable adenylate
7	61	69.3	253	2 B81706	adenylate kinase T
8	60	68.2	215	2 G83184	adenylate kinase P
9	60	68.2	232	2 JC5893	adenylate kinase (
10	60	68.2	239	2 G02248	adenylate kinase (
11	60	68.2	239	2 J01944	adenylate kinase (
12	60	68.2	248	2 S44766	adenylate kinase (
13	59	67.0	214	1 K7ECA	adenylate kinase (
14	59	67.0	214	2 S70734	adenylate kinase (
15	59	67.0	214	2 C82255	adenylate kinase V
16	59	67.0	214	2 AC0378	adenylate kinase (
17	59	67.0	214	2 AC0563	adenylate kinase (
18	59	67.0	214	2 C85545	adenylate kinase (
19	59	67.0	214	2 G90694	adenylate kinase (
20	59	67.0	215	2 S61841	adenylate kinase (
21	59	67.0	215	2 S61843	adenylate kinase (
22	59	67.0	215	2 B84986	adenylate kinase (
23	59	67.0	215	2 F81154	adenylate kinase N
24	59	67.0	234	2 B29792	adenylate kinase (
25	59	67.0	241	2 JS0422	adenylate kinase (
26	57	64.8	205	2 S17070	adenylate kinase (
27	56	63.6	181	2 B87138	probable adenylate
28	56	63.6	181	2 T45390	adenylate kinase (
29	56	63.6	213	2 D86521	adenylate kinase (

30	56	63.6	213	2 H72100	adenylate kinase C
31	56	63.6	214	2 I64062	adenylate kinase (
32	55	62.5	43	2 I40341	adenylate kinase (
33	55	62.5	215	2 A81777	adenylate kinases
34	55	62.5	215	2 A81777	adenylate kinases
35	54	61.4	70	2 PC4087	adenylate kinases
36	54	61.4	176	2 G70658	adenylate kinase (
37	54	61.4	187	2 S77483	probable aroK prot
38	54	61.4	194	2 AD3349	adenylate kinase (
39	54	61.4	199	2 PC4230	adenylate kinase (
40	54	61.4	205	2 S50007	adenylate kinase (
41	54	61.4	214	2 I64218	adenylate kinase (
42	54	61.4	218	2 S43016	adenylate kinase (
43	54	61.4	222	1 K1BYA	adenylate kinase (
44	53	60.2	177	2 H97205	probable kinase fr
45	53	60.2	181	2 H70822	probable adenylate

## ALIGNMENTS

RESULT 1  
J01945  
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - rat  
N:Alternate names: GTP-AMP phosphotransferase AK3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
C:Accession: J01945  
R:Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.  
J. Biochem. 113, 200-207, 1993  
A:Title: Tissue-specific and developmentally regulated expression of the genes encodi  
A:Reference number: P00534; MUID:93224500; PMID:4468325  
A:Accession: J01945  
A:Molecule type: mRNA  
A:Residues: 1-227 <TAN>  
A:Cross-references: DDBJ:D13062; NID:q220797; PIDN:BA02379.1; PID:q450312  
A:Superfamily: adenylate kinase  
K:Keywords: ATP; GTP; mitochondrion; nucleotide binding; P-loop; phosphotransferase  
F:14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 95.5%; Score 84; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLRRAVIMGAPSGSGKT 17  
Db 6 RLRRAVIMGAPSGSGKT 22  
|||||  
|||||

RESULT 2  
A34442  
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine  
N:Alternate names: adenylate kinase 3  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 03-Jun-2002  
C:Accession: A34442; JH0512; A24201  
R:Yamada, M.; Shahjahan, M.; Tanabe, T.; Kishi, F.; Nakazawa, A.  
J. Biol. Chem. 264, 19192-19199, 1989  
A:Title: Cloning and characterization of cDNA for mitochondrial GTP-AMP phosphotransf  
A:Reference number: A34442; MUID:90037053; PMID:2478555  
A:Accession: A34442  
A:Molecule type: mRNA  
A:Residues: 1-227 <YAM>  
A:Cross-references: GB:M05757; NID:q163527; PIDN:AAA30705.1; PID:q163528  
R:Shahjahan, M.; Yamada, M.; Tanaka, H.; Nakazawa, A.  
Gene 107, 313-317, 1991  
A:Title: Cloning and characterization of the gene encoding bovine mitochondrial adeny  
A:Reference number: JH0512; MUID:92084124; PMID:1748300  
A:Accession: JH0512  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-50 <SHA>  
R:Tomaselli, A.G.; Frank, R.; Schiltz, E.

EMBL Lett. 202,303-308, 1986  
 A:Title: The complete primary structure of GMP:AMP phosphotransferase from beef heart m  
 A:Reference number: A24201, MUID:86248102, PMID:3013690  
 A:Accession: A24201..  
 A:Molecule type: protein  
 A:Residues: 2-10,12-227 <TOM>  
 C:Genetics:  
 A:Gene: AK3  
 A:Introns: 51/1; 91/1; 148/3; 188/2  
 C:Superfamily: adenylate kinase  
 C:Keywords: ATP: mitochondrion; nucleotide binding; P-loop; phosphotransferase  
 F:2-227/Product: GTP-AMP phosphotransferase, mitochondrial #status predicted <MAT>  
 F:14-21/Region: nucleotide-binding motif A (P-loop)  
  
 Query Match 95.5%; Score 84; DB 2; Length 227;  
 Best Local Similarity 94.4%; Pred. No. 0.00012;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 RLLRAVINGAPGSGKGTV 18  
 ||||| |||||  
 DB 6 RLLRAVINGAPGSGKGTV 23

```

RESULT 3
KIHUA3
nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human
N:Alternate names: adenylate kinase 3
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 23-Mar-1995 #text_change 03-Jun-2002
C:Accession: A42820; S16380; S16381
R:Xu, G.; O'Connell, P.; Stevens, J.; White, R.
Genomics 13, 537-542, 1992
A:Title: Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3
A:Reference number: A42820; MUID:92347846; PMID:1639383
A:Accession: A42820
A:Molecule type: mRNA
A:Residues: 1-223 <XUG>
A:Cross-references: EMBL:X60673; NID:g28576; PIND:CAA43088.1; PID:g28577; GB:S41502
A:Experimental source: frontal cortex
A:Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIPI:109645)
C:Comment: This isozyme is found in the mitochondrial matrix.
C:Genetics:
A:Gene: GDB:AK3
A:Cross-references: GDB:118988; OMIM:103030
A:Map position: 9pter-p13
C:Function:
A:Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu
A:Note: GTP is preferred to ATP as a substrate
C:Superfamily: adenylate kinase
C:Keywords: ATP; mitochondrial matrix; mitochondrion; P-loop; phosphotransferase
F:12-19/Region: nucleotide-binding motif A (P-loop) #status atypical
F:85-89/Region: nucleotide-binding motif B #status atypical
F:22,33,35,88/Active site: Cys, His, Ser, Asp #status predicted

Query Match      87.5%  Score 77;  DB 1;  Length 223;
Best Local Similarity 83.3%, Pred. No. 0.0012;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  RLRAVINGARGSGKGTV 18
          :|:|:|:|:|:|:|:|:|
DB      4  RLRAVILGPPGSGKGTV 21

RESULT 4
B82825
adenylate kinase XF0275 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: B82825
R:anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347

```

A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: B82875  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-198 <SIM>  
A:Cross-references: GB:AE003881; GB:AE003849; NID:9105093; PIDN:AMF83088.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
B:Rios, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carter  
as-Neto, E.; Docena, C.; El-Dorri, H.; Falcicant, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; France, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF0275  
C:Superfamily: adenylate kinase  
Query Match 70.5% Score 62; DB 2; Length 198;  
Best Local Similarity 68.8% Pred. No. 0.13;  
Matches 11; Conservative 3; Mismatches 0; Indels 2; Gaps 0;

OY 2 LIRAVIMGAPSGKCT 17  
| : | : | | | | |  
DB 11 LMRLVLLGPPGSGKCT 26

RESULT 5  
S23568  
adenylate kinase (EC 2.7.4.3) ADK2 - yeast (*Saccharomyces cerevisiae*)  
N.Alternate names: PAK3 protein; Protein YER170W  
C.Species: *Saccharomyces cerevisiae*  
C.Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 19-Jan-2001  
A.Accession: S23568; JCI1335; S50673  
R.Schricker, R.; Magdalen, V., Bandlow, W.  
Mol. Gen. Genet. 233, 363-371, 1992  
A>Title: A new member of the adenylate kinase family in yeast: PAK3 is highly homologous to the yeast adenylate kinase  
A.Reference number: S23568; MUID:92318888; PMID:1620094  
A.Accession: S23568  
A.Molecule type: DNA  
A.Residues: 1-225 <SCH>  
A.Cross-references: EMBL:X65126; NID:g4096; PIDN:CAA46254.1; PID:g4097  
R.Cooper, A.J.; Friedberg, E.C.  
Gene 114, 145-148, 1992  
A>Title: A putative second adenylate kinase-encoding gene from the yeast *Saccharomyces cerevisiae*  
A.Reference number: JCI1335; MUID:92267376; PMID:1587477  
A.Accession: JCI1335  
A>Status: nucleic acid sequence not shown  
A.Molecule type: DNA  
A.Residues: 1-225 <COO>  
A.Cross-references: GB:M77757; NID:g171045; PIDN:AAA34418.1; PID:g171046  
R.Dietrich, F.S.  
submitted to the EMBL Data Library, December 1994  
A.Description: The sequence of *S. cerevisiae* cosmids 9163 and 9132.  
A.Reference number: S50673  
A.Accession: S50673  
A.Molecule type: DNA  
A.Residues: 1-225 <DIE>  
A.Cross-references: EMBL:U18922; NID:g603405; PIDN:AAB64697.1; PID:g603411; MIPS:YER1  
C.Genetics:  
A.Gene: SGD:ADK2; PAK3  
A.Cross-references: SGD:S0000972; MIPS:YER170W  
A.Map position: 5R  
C.Function:  
A.Description: phosphotransferase  
C:Superfamily: adenylate kinase

C:Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase  
F:21-28/Region: nucleotide-binding motif A (P-loop)

Query Match 70.5%; Score 62; DB 2; Length 225;  
Best Local Similarity 73.3%; Pred. No. 0.15;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17  
|| :|||:|||||  
DB 15 LRLLLGAPGSGKGT 29

RESULT 6  
D71554  
probable adenylate cyclase - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C>Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 24-Nov-1999  
C:Accession: D71554

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: D71554  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-245 <ARN>  
A:Cross-references: GB:AE001286; GB:AE001273; NID:g3328516; PIDN:AA67719.1; PID:g332852  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: adk  
C:Superfamily: adenylate kinase

Query Match 69.3%; Score 61; DB 2; Length 245;  
Best Local Similarity 91.7%; Pred. No. 0.23;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VINGAPGSGKGT 17  
:|||||  
DB 9 IIMGAPGSGKGT 20

RESULT 7  
B81706  
adenylate kinase TC0404 [Imported] - Chlamydia muridarum (strain N199)  
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Jun-2000  
C:Accession: B81706

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.  
A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: B81706  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-253 <TEB>  
A:Cross-references: GB:AE002307; GB:AE002160; NID:g7190442; PIDN:AAF39261.1; PID:g719044  
A:Experimental source: strain N199 (Mopn)  
C:Genetics:  
A:Gene: TC0404  
C:Superfamily: adenylate kinase

Query Match 69.3%; Score 61; DB 2; Length 253;  
Best Local Similarity 91.7%; Pred. No. 0.23;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VINGAPGSGKGT 17  
:|||||  
DB 9 IIMGAPGSGKGT 20

RESULT 8  
G83184

adenylate kinase PA3686 [Imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: G83184

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yvan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: G83184  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-215 <STO>

A:Cross-references: GB:AE004788; GB:AE004091; NID:g9949846; PIDN:AA607074.1; GSPDB:GN1  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: adk; PA3686  
C:Superfamily: adenylate kinase

Query Match 68.2%; Score 60; DB 2; Length 215;  
Best Local Similarity 60.0%; Pred. No. 0.27;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17  
:|||||  
DB 1 MRVILGAPGAGKGT 15

RESULT 9  
JC5893  
adenylate kinase (EC 2.7.4.3) 2B - human  
N:Alternate names: ATP-AMP transphosphorylase  
C:Species: Homo sapiens (man)  
C>Date: 18-Mar-1998 #sequence\_revision 18-Mar-1998 #text\_change 18-Jun-1999  
C:Accession: JC5893

R:Lee, Y.; Kim, J.W.; Lee, S.M.; Kim, H.J.; Lee, K.S.; Park, C.; Choe, I.S. J. Biochem. 123, 47-54, 1998  
A:Title: Cloning and expression of human adenylate kinase 2 isozymes: Differential expression of human adenylate kinase 2 isozymes: Differential expression  
A:Reference number: JC5893; MUID:98162934; PMID:9504408  
A:Accession: JC5893  
A:Molecule type: mRNA  
A:Residues: 1-232 <LEB>

A:Cross-references: GB:U54645; NID:g1710886; PIDN:AA13881.1; PID:g1477653  
A:Experimental source: Ussue fetal liver  
C:Comment: This key enzyme is involved in energy metabolism.  
C:Genetics:  
A:Gene: adk2b  
C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP  
A:Note: magnesium required  
C:Superfamily: adenylate kinase  
C:Keywords: alternative splicing; ATP; P-loop; phosphotransferase  
F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical  
F:95-100/Region: nucleotide-binding motif B #status atypical  
F:42-92/Dsulfide bonds: #status predicted  
F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 68.2%; Score 60; DB 2; Length 232;  
Best Local Similarity 66.7%; Pred. No. 0.3;  
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17  
:|||||  
DB 16 IRVILLGPPGAGKGT 30

RESULT 10  
G02248  
adenylate kinase (EC 2.7.4.3) 2 - human  
N:Alternate names: ATP-AMP transphosphorylase  
C:Species: Homo sapiens (man)  
C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 18-Jun-1999



submitted to the Brookhaven Protein Data Bank, February 1994

A:Reference number: A52276; PDB:1ANK

A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-214

C:Genetics:

A:Gene: adk; plsa; dnaW

A:Map position: 11 min

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30-84/Active site: Ser, Asp #status predicted

Query Match 67.0%; Score 59; DB 1; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVIMGAPGSGKGT 17  
:|:::|||||  
DB 1 MRLILGAPGAGKGT 15

#### RESULT 14

S70734

adenylate kinase (EC 2.7.4.3) - Yersinia enterocolitica

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Yersinia enterocolitica

C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999

C:Accession: S70734; S51258

R:Skurnik, M.; Venho, R.; Tolvanen, P.; Al-Hendy, A.

Mol. Microbiol. 17, 575-594, 1995

A:Title: A novel locus of Yersinia enterocolitica serotype O:3 involved in lipopolysacch

A:Reference number: S70734; MUID:96100456; PMID:8559076

A:Accession: S70734

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-214 <SKU>

A:Cross-references: EMBL:247767; NID:9633689; PIDN:CAA87696.1; PID:9633690

A:Experimental source: strain 6471/76 serotype O:3

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C:Genetics:

A:Gene: adk

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:126/Active site: His #status predicted

Query Match 67.0%; Score 59; DB 2; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVIMGAPGSGKGT 17  
:|:::|||||  
DB 1 MRLILGAPGAGKGT 15

#### RESULT 15

C82255

adenylate kinase VC0986 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: C82255

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers, F

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-214 <HE1>

A:Cross-references: GB:AE004180; GB:AE003852; NID:99655445; PIDN:AAF94147.1; GSPDB:GN

A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:

A:Gene: VC0986

A:Map position: 1

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30-84/Active site: Ser, Asp #status predicted

Query Match 67.0%; Score 59; DB 2; Length 214;

Best Local Similarity 60.0%; Pred. No. 0.38;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 LRAVIMGAPGSGKGT 17  
:|:::|||||  
DB 1 MRLILGAPGAGKGT 15

Search completed: April 24, 2003, 10:20:18  
Job time : 44 secs



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 15 Seconds  
(Without alignments)  
35.308 Million cell updates/sec

Title: US-10-006-190-1\_COPY\_6\_23  
Perfect score: 88  
Sequence: 1 RLRAVIMGAPSGSGKGTV 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_CA:\*

- 1: /cgn2\_6/ptodata/1/laa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/laa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/laa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/laa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/laa/PCTUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/laa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	227	2 US-08-829-027-1	Sequence 1, Appl1
2	88	100.0	227	3 US-09-225-366-1	Sequence 1, Appl1
3	88	100.0	227	4 US-09-149-476-377	Sequence 377, App
4	84	95.5	227	2 US-08-829-027-3	Sequence 3, Appl1
5	84	95.5	227	2 US-08-829-027-4	Sequence 4, Appl1
6	84	95.5	227	3 US-09-225-366-3	Sequence 3, Appl1
7	84	95.5	227	3 US-09-225-366-4	Sequence 4, Appl1
8	84	95.5	227	3 US-08-829-027-5	Sequence 5, Appl1
9	77	87.5	223	3 US-09-225-366-5	Sequence 5, Appl1
10	58	65.9	438	4 US-08-915-4988-37	Sequence 37, Appl1
11	52	59.1	222	4 US-09-134-001C-3289	Sequence 3289, Ap
12	50	56.8	197	2 US-08-879-561-5	Sequence 5, Appl1
13	49	55.7	194	2 US-08-879-561-11	Sequence 11, Appl1
14	49	55.7	194	2 US-08-879-561-12	Sequence 12, Appl1
15	48	54.5	282	4 US-09-222-939-17	Sequence 17, Appl1
16	48	54.5	288	4 US-09-134-001C-4963	Sequence 4963, Ap
17	46	52.3	1463	4 US-08-157-005-3	Sequence 3, Appl1
18	46	52.3	1463	4 US-08-747-863-3	Sequence 3, Appl1
19	46	52.3	1463	4 US-09-565-864-3	Sequence 3, Appl1
20	45	51.1	283	4 US-09-222-939-2	Sequence 2, Appl1
21	45	51.1	2517	2 US-08-801-263A-5	Sequence 5, Appl1
22	45	51.1	2517	3 US-09-102-248-5	Sequence 5, Appl1
23	43	48.9	539	2 US-08-759-581B-20	Sequence 20, Appl1
24	43	48.9	539	4 US-09-304-711-20	Sequence 20, Appl1
25	43	48.9	539	4 US-09-173-281-20	Sequence 20, Appl1
26	43	48.9	1065	3 US-08-630-172-9	Sequence 9, Appl1
27	43	48.9	1065	4 US-09-375-419-9	Sequence 9, Appl1

28	43	48.9	1170	2 US-08-789-078-2	Sequence 2, Appl1
29	43	48.9	1170	2 US-08-752-633-2	Sequence 2, Appl1
30	43	48.9	1170	2 US-08-476-062A-42	Sequence 42, Appl1
31	43	48.9	1170	5 PCT-US95-04886-2	Sequence 2, Appl1
32	43	48.9	1170	5 PCT-US96-01314-42	Sequence 42, Appl1
33	43	48.9	3457	2 US-08-416-603-4	Sequence 4, Appl1
34	42	47.7	297	2 US-09-006-535-4	Sequence 4, Appl1
35	42	47.7	298	2 US-09-006-535-3	Sequence 3, Appl1
36	42	47.7	388	2 US-08-759-581B-9	Sequence 9, Appl1
37	42	47.7	388	4 US-09-304-711-9	Sequence 9, Appl1
38	42	47.7	388	4 US-09-173-281-9	Sequence 9, Appl1
39	42	47.7	475	4 US-09-212-247C-4	Sequence 4, Appl1
40	42	47.7	694	2 US-08-895-522-4	Sequence 4, Appl1
41	42	47.7	694	3 US-09-195-381-4	Sequence 4, Appl1
42	42	47.7	1408	1 US-08-612-521-2	Sequence 2, Appl1
43	42	46.6	311	4 US-09-134-001C-4471	Sequence 4471, Ap
44	41	46.6	311	2 US-08-775-009-33	Sequence 33, Appl1
45	41	46.6	318	2 US-08-671-947-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-829-027-1  
Sequence 1, Application US/08829027  
Patent No. 5856160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,027  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PR-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 2122022  
US-08-829-027-1  
Query Match 100.0%; Score 88; DB 2; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 1 RLRAVIMGAPSGSGKTIV 18  
Db 6 RLRAVIMGAPSGSGKTIV 23

## RESULT 2

US-09-225-366-1  
; Sequence 1, Application US/09225366  
; Patent No. 6001624  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purni  
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/225,366  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/829,027  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0256 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 227 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: 2122022  
US-09-225-366-1

Query Match 100.0%; Score 88; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKTIV 18  
Db 6 RLRAVIMGAPSGSGKTIV 23

## RESULT 3

US-09-149-476-377  
; Sequence 377, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11



EARLIER APPLICATION NUMBER: 60/043, 669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048, 974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056, 886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 637  
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EARLIER APPLICATION NUMBER: 60/056, 903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 880  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047, 595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 594

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047, 501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056, 632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057, 650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056, 884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 88; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 1, 1e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLRAVINGAPSGKGV 18  
|||||  
Db 6 RLRAVINGAPSGKGV 23

RESULT 4  
US-08-829-027-3  
Sequence 3, Application US/08829027  
Patent No. 5856160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette



|||||  
Db 6 RLRAVIMGAPSGKGT 23

RESULT 7  
US-09-225-366-4  
Sequence 4, Application US/09225366  
Patent No. 6001624  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,366  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/829,027  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 227 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 450312  
US-09-225-366-4  
Query Match 95.5%; Score 84; DB 3; Length 227;  
Best local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLRAVIMGAPSGKGT 17  
Db 6 RLRAVIMGAPSGKGT 22  
RESULT 8  
US-08-829-027-5  
Sequence 5, Application US/08829027  
Patent No. 5856160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,027  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 28577  
US-08-829-027-5

Query Match 87.5%; Score 77; DB 2; Length 223;  
Best local Similarity 83.3%; Pred. No. 0.00044;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPSGKGT 18  
Db 4 RLRAVIMGAPSGKGT 21

RESULT 9  
US-09-225-366-5  
Sequence 5, Application US/09225366  
Patent No. 6001624  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,366  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/829,027  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 28577  
US-09-225-366-5

Query Match 87.5%; Score 77; DB 3; Length 223;  
Best Local Similarity 83.3%; Pred. No. 0.00044;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKTV 18  
Db 4 KLRVAVILGPPGSGKTV 21

RESULT 10  
US-08-915-4988-37  
Sequence 37, Application US/089154988  
Patent No. 6132954  
GENERAL INFORMATION:  
APPLICANT: James R. Lupski, Robert A. Britton, Donald L.  
TITLE OF INVENTION: Methods of Screening for Agents that  
TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
ADDRESS: 8 No. 6132954Tis LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT for WINDOWS 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,4988  
FILING DATE: August 20, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: 60/023,353  
APPLICATION NUMBER: 60/023,353  
FILING DATE: August 20, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Lori Y. Beardsell  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: BYLR-0037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-915-4988-37

Query Match 65.9%; Score 58; DB 4; Length 438;

Best Local Similarity 55.6%; Pred. No. 0.5;  
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLRAVIMGAPGSGKTV 18  
Db 113 RLRAVILGAPNAGKSTL 130

RESULT 11  
US-09-134-001C-3289  
Sequence 3289, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3289  
LENGTH: 222  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3289

Query Match 59.1%; Score 52; DB 4; Length 222;  
Best Local Similarity 53.3%; Pred. No. 1.9;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LRAVIMGAPGSGKGT 17  
Db 8 MWITLMLGPPGSGKGT 22

RESULT 12  
US-08-879-561-5  
Sequence 5, Application US/08879561  
Patent No. 5817482  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hallman, Jennifer L.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/879,561  
FILING DATE: Herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0325 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: CORPNOT02  
CLONE: 1484821  
US-08-879-561-5

Query Match 56.8%; Score 50; DB 2; Length 197;  
Best Local Similarity 81.8%; Pred. No. 3.3;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17  
Db 16 IIGGPGSGKGT 26

RESULT 13  
US-08-879-561-11  
Sequence 11, Application US/08879561  
Patent No. 5817482  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
CLASSIFICATION: 424  
FILING DATE: Herewith  
APPLICATION NUMBER: US/08/879,561  
PRIOR APPLICATION DATA:  
CLASSIFICATION: 424  
FILING DATE: Herewith  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0325 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-879-561-11

Query Match 55.7%; Score 49; DB 2; Length 194;

Best Local Similarity 72.7%; Pred. No. 4.5;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17  
Db 13 VVGPGSGKGT 23

RESULT 14  
US-08-879-561-12  
Sequence 12, Application US/08879561  
Patent No. 5817482  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
CLASSIFICATION: 424  
FILING DATE: Herewith  
APPLICATION NUMBER: US/08/879,561  
PRIOR APPLICATION DATA:  
CLASSIFICATION: 424  
FILING DATE: Herewith  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0325 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-879-561-12

Query Match 55.7%; Score 49; DB 2; Length 194;  
Best Local Similarity 72.7%; Pred. No. 4.5;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 IMGAPGSGKGT 17  
Db 14 VVGPGSGKGT 24

RESULT 15  
US-09-222-939-17  
Sequence 17, Application US/09222939  
Patent No. 6372448  
GENERAL INFORMATION:  
APPLICANT: Fritz, Christian  
APPLICANT: Youngman, Phillip  
APPLICANT: Guzman, Luz-Marie  
TITLE OF INVENTION: USE OF YLOF, YQEG, YVBO, YERL, AND YSXC, ESSENTIAL BACTERIAL

```

; TITLE OF INVENTION: GENES AND POLYPEPTIDES
; FILE REFERENCE: 07334/111001
; CURRENT APPLICATION NUMBER: US/09/222,939
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 17
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-222-939-17

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Query Match          54.5%; Score 48; DB 4; Length 282;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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QY 1 RLRAVIMGAPGSGKTV 18
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Db 119 RAIRALIIGIPVGSSTL 136

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Search completed: April 24, 2003, 10:20:40  
 Job time : 16 secs

GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 35 seconds

(without alignments)  
68.529 Million cell updates/sec

Title: US-10-006-190-1\_COPY\_6\_23

Perfect score: 88

Sequence: 1 RLLRAVIMGAPGSGKTV 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	227	19	AAW81101 Human mitochondria
2	88	100.0	227	19	AAW74787 Human secreted pro
3	88	100.0	227	21	AAW12440 Human mitochondria
4	88	100.0	227	22	AAW38899 Human polypeptide
5	88	100.0	227	22	AAW92887 Human protein sequ
6	88	100.0	227	22	AAW93066 Human protein sequ
7	88	100.0	227	22	AAW93487 Human protein sequ
8	88	100.0	227	22	AAW85885 Human adenylate ki
9	88	100.0	227	22	AAW12326 Human secreted pro
10	88	100.0	227	22	AAW40685 Human polypeptide

11	88	100.0	256	22	AAW3865 Human colon cancer
12	84	95.5	227	21	AAW12441 AK3 protein sequen
13	77	87.5	224	22	AAW11778 Human kinase (PKIN
14	74	84.1	216	22	AAW62530 Drosophila melanog
15	70	79.5	214	21	AAW53619 Human colon cancer
16	64	72.7	203	22	AAW42464 Propionibacterium
17	62	70.5	335	22	AAW23968 Novel human diago
18	61	69.3	245	20	AAW37077 Protein involved i
19	60	68.2	106	21	AAW01367 Human secreted pro
20	60	68.2	215	22	AAW36349 Pseudomonas aerugi
21	60	68.2	232	20	AAW77257 Human adenylate ki
22	60	68.2	237	23	AAW41753 Human ovarian anti
23	60	68.2	238	22	AAW19263 Novel human diago
24	59	67.0	214	22	AAW34482 E. coli cellular p
25	59	67.0	214	22	AAW36040 Klebsiella pneumon
26	59	67.0	214	22	AAW38124 Salmonella typhi c
27	58	67.0	648	22	AAW26095 Novel human diago
28	58	65.9	86	22	AAW99570 ERA binding domain
29	58	65.9	158	21	AAW02190 Human secreted pro
30	58	65.9	342	21	AAW56160 Human secreted pro
31	58	65.9	437	20	AAW28519 Human regulatory p
32	58	65.9	437	22	AAW40298 Human polypeptide
33	58	65.9	437	22	AAW94547 Human protein sequ
34	58	65.9	438	22	AAW35620 Human ERA protein.
35	58	65.9	443	22	AAW42084 Human polypeptide
36	57	64.8	215	23	AAW48830 Listeria monocytog
37	57	64.8	237	22	AAW59655 Drosophila melanog
38	56	63.6	214	22	AAW35415 Haemophilus Influe
39	56	63.6	224	22	AAW36634 Staphylococcus aur
40	56	63.6	224	22	AAW37231 Staphylococcus aur
41	55	62.5	74	22	AAW43756 Peptide #11262 enc
42	55	62.5	74	22	AAW77489 Human bone marrow
43	55	62.5	74	22	AAW21416 Peptide #7850 enco
44	55	62.5	74	22	AAW37653 Peptide #11690 enc
45	55	62.5	74	23	AAW46511 Human peptide enco

## ALIGNMENTS

RESULT 1	
AAW81101	
ID	AAW81101 standard; Protein; 227 AA.
AC	AAW81101;
DT	29-JAN-1999 (first entry)
DE	Human mitochondrial adenylate kinase protein.
XX	
KW	Human; mitochondrial; adenylate kinase; therapeutic;
KW	neurological disorder; Alzheimer; Huntington; epilepsy; cancer;
KW	neural; inflammation; immune.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Misc-difference 182
FT	Location/Qualifiers
FT	/note="Xaa is unspecified, encoded by NCA"
FT	Misc-difference 185
FT	/note="Xaa is unspecified, encoded by GMA"
XX	
PN	WO9844124-A1.
XX	
PD	08-OCT-1998.
XX	
PF	30-MAR-1998; 98WC-US06249.
XX	
PR	31-MAR-1997; 97US-0829027.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Hillman JL, Shah P;

XX WPI: 1998-557119/47.  
DR N-PSDB; AAV68223.  
XX  
PT Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat  
PT neurological disorders such as Alzheimer's and screen for  
PT antagonists for treatment of cancer or immunological disorders  
XX  
PS Claim 5; Fig 1; 63pp; English.  
XX  
CC The human mitochondrial adenylate kinase (HMAK) protein of 227 amino  
CC acids ) can be administered therapeutically, especially by expressing  
CC encoding polypeptides, to treat neurological disorders e.g. Alzheimer's  
CC disease, Huntington's disease, epilepsy. It can be combined with a  
CC suitable carrier in pharmaceutical compositions, which can be  
CC administered to treat such disorders. HMAK was shown to have chemical  
CC and structural homology with adenylate kinase isozyme 3 (AK3) from cow,  
CC rat and human (92, 91 and 57 % identity respectively) and was expressed  
CC in e.g. cancerous tissues, brain and neural tissues and tissues involved  
CC in inflammation and the immune response. Increased activity or  
CC expression was proposed to be associated with cancer and immunological  
CC disorders, and decreased activity/expression with the development of  
CC neurological disorders. Products of the above invention may be used in  
CC the diagnosis and treatment of the above diseases and disorders.  
XX  
SQ Sequence 227 AA:  
  
Query Match 100.0%; Score 88; DB 19; Length 227;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RLRAVIMGAPSGSKGV 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 RLRAVIMGAPSGSKGV 23  
  
RESULT 2  
AAW74787  
ID AAW74787 standard: Protein; 227 AA.  
XX  
AC AAW74787;  
XX  
DE 19-JAN-1999 (first entry)  
XX  
DE Human secreted protein encoded by gene 58 clone HHRHN61.  
XX  
KW Human; secreted protein; testis; tumour; foetal brain tissue;  
KW fusion protein; cancer; central nervous system; seizure;  
KW diagnosis; neurodegenerative disease.  
XX  
XX Homo sapiens.  
OS  
PN MO9839448-A2.  
PD 11-SEP-1998.  
XX  
PF 06-MAR-1998; 98MO-US04493.  
XX  
PR 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0036221.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 11-APR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043314.  
PR 11-APR-1997; 97US-0043568.  
PR 11-APR-1997; 97US-0043569.

PR 11-APR-1997; 97US-0043576.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043669.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0047492.  
PR 23-MAY-1997; 97US-0047500.  
PR 23-MAY-1997; 97US-0047501.  
PR 23-MAY-1997; 97US-0047502.  
PR 23-MAY-1997; 97US-0047503.  
PR 23-MAY-1997; 97US-0047581.  
PR 23-MAY-1997; 97US-0047582.  
PR 23-MAY-1997; 97US-0047583.  
PR 23-MAY-1997; 97US-0047584.  
PR 23-MAY-1997; 97US-0047585.  
PR 23-MAY-1997; 97US-0047586.  
PR 23-MAY-1997; 97US-0047587.  
PR 23-MAY-1997; 97US-0047588.  
PR 23-MAY-1997; 97US-0047589.  
PR 23-MAY-1997; 97US-0047590.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047593.  
PR 23-MAY-1997; 97US-0047594.  
PR 23-MAY-1997; 97US-0047595.  
PR 23-MAY-1997; 97US-0047596.  
PR 23-MAY-1997; 97US-0047597.  
PR 23-MAY-1997; 97US-0047598.  
PR 23-MAY-1997; 97US-0047599.  
PR 23-MAY-1997; 97US-0047600.  
PR 23-MAY-1997; 97US-0047601.  
PR 23-MAY-1997; 97US-0047612.  
PR 23-MAY-1997; 97US-0047613.  
PR 23-MAY-1997; 97US-0047614.  
PR 23-MAY-1997; 97US-0047615.  
PR 23-MAY-1997; 97US-0047617.  
PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
PR 23-MAY-1997; 97US-0047633.  
PR 06-JUN-1997; 97US-0048864.  
PR 06-JUN-1997; 97US-0048874.  
PR 13-JUN-1997; 97US-0048610.  
PR 08-JUL-1997; 97US-0051926.  
PR 16-JUL-1997; 97US-0052874.  
PR 18-AUG-1997; 97US-0055724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056862.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.  
PR 22-AUG-1997; 97US-0056874.  
PR 22-AUG-1997; 97US-0056875.  
PR 22-AUG-1997; 97US-0056876.  
PR 22-AUG-1997; 97US-0056877.  
PR 22-AUG-1997; 97US-0056878.  
PR 22-AUG-1997; 97US-0056879.  
PR 22-AUG-1997; 97US-0056880.  
PR 22-AUG-1997; 97US-0056881.  
PR 22-AUG-1997; 97US-0056882.  
PR 22-AUG-1997; 97US-0056884.  
PR 22-AUG-1997; 97US-0056886.  
PR 22-AUG-1997; 97US-0056887.  
PR 22-AUG-1997; 97US-0056888.  
PR 22-AUG-1997; 97US-0056889.  
PR 22-AUG-1997; 97US-0056892.



PR 22-AUG-1997; 97US-0056893.  
 PR 22-AUG-1997; 97US-0056894.  
 PR 22-AUG-1997; 97US-0056903.  
 PR 22-AUG-1997; 97US-0056908.  
 PR 22-AUG-1997; 97US-0056909.  
 PR 22-AUG-1997; 97US-0056910.  
 PR 22-AUG-1997; 97US-0056911.  
 PR 05-SEP-1997; 97US-0056915.  
 PR 05-SEP-1997; 97US-0057669.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
 PI Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 XX  
 DR WPI: 1998-506364/43.  
 DR N-PSDB: AAV59568.  
 XX  
 PR New isolated human genes and the secreted polypeptide(s) they encode  
 PR - useful for diagnosis and treatment of e.g. cancers, neurological  
 PR disorders, immune diseases, inflammation or blood disorders  
 XX  
 PS Claim 1: Page 575-576; 721pp; English.  
 XX  
 CC This sequence represents a secreted human protein encoded by the nucleic  
 CC acid molecule designated Gene 58 from the human cDNA clone HHEH61  
 CC (deposited as clone ATCC 97899 and ATCC 209045).  
 CC The gene can be used to generate fusion proteins by linking to the gene  
 CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the  
 CC stability of the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W5026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses).  
 CC  
 XX  
 SQ Sequence 227 AA:  
 Query Match 100.0%; Score 88; DB 19; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLLRAVINGAPSGSGKTV 18  
 DB 6 RLLRAVINGAPSGSGKTV 23  
 RESULT 3  
 AABI2440  
 ID AABI2440 standard; Protein: 227 AA.  
 XX  
 AC AABI2440;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4.  
 XX  
 KW Human: mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.  
 KW  
 OS Homo sapiens.  
 XX  
 XX CN1249340-A.  
 PN  
 PI 05-APR-2000.  
 PD  
 XX

PF 28-SEP-1998; 98CN-0119439.  
 XX  
 PR 28-SEP-1998; 98CN-0119439.  
 XX  
 PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.  
 XX  
 PI Yu L, Zhao Y, Bi A;  
 XX  
 DR WPI: 2000-400718/35.  
 DR N-PSDB: AAA60582.  
 XX  
 PR Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,  
 PR its encode sequence -  
 XX  
 PS Claim 4: Page 14-15; 20pp; Chinese.  
 XX  
 CC The present invention describes a new ribotide sequence of human gene,  
 CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP  
 CC phosphotransferase (GTP3P) and the encoded polypeptide. The present  
 CC sequence represents human GTP3P.  
 CC  
 XX  
 SQ Sequence 227 AA:  
 Query Match 100.0%; Score 88; DB 21; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLLRAVINGAPSGSGKTV 18  
 DB 6 RLLRAVINGAPSGSGKTV 23  
 RESULT 4  
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 ID AAM38899 standard; Protein: 227 AA.  
 XX  
 AC AAM38899;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 2044.  
 XX  
 KW Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 WPI: 2001-442253/47.

DR	N-PSDB:AA158055.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
XX	
XX	Example 3: SEQ ID NO 2044; 10078bp; English.
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AA038642-AA042213) with neurotropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilization of the activities such as: immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
XX	
SQ	Sequence 227 AA:
Query Match	100.0%; Score 88; DB 22; Length 227;
Best Local Similarity	100.0%; Pred. No. 0.0001;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RLLRAVIMGAPSGSGKTV 18
DB	6 RLLRAVIMGAPSGSGKTV 23
RESULT 5	
AA092887	
ID	AA092887 standard; Protein; 227 AA.
XX	
XX	AA092887;
DT	26-JUN-2001 (first entry)
XX	
DE	Human protein sequence SEQ ID NO:11492..
XX	
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX	
OS	Homo sapiens.
XX	
XX	EP1074617-A2.
PN	
XX	
PD	07-FEB-2001.
XX	
XX	28-JUL-2000; 2000EP-0116126.
XX	
XX	29-JUL-1999; 99JP-0248036.
PR	27-AUG-1999; 99JP-0300253.
PR	11-JAN-2000; 2000JP-0118776.
PR	02-MAY-2000; 2000JP-0183767.
PR	09-JUN-2000; 2000JP-0241899.
XX	
PA	(HELI-) HELIX RES INST.
XX	
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI	Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
XX	
XX	WPI; 2001-318749/34.
PT	Primer sets for synthesizing polynucleotides, particularly the 5602
PT	full-length cDNAs defined in the specification, and for the detection
PT	and/or diagnosis of the abnormality of the proteins encoded by the
PT	full-length cDNAs -
XX	

PS	Claim 8:	SEQ ID 11492;	2537bp + CD ROM; English.
XX			
CC	The present invention describes primer sets for synthesizing 5602		
CC	full-length cDNAs defined in the specification, where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNAs easily without any specialised methods. AAH0316 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to		
CC	AAB935893 represent human amino acid sequences; and AAH13629 to AAH13632		
CC	represent oligonucleotides, all of which are used in the exemplification		
CC	of the present invention.		
SQ			
SQ	Sequence      227 AA;		
	Query Match            100.0%; Score 88; DB 22; Length 227;		
	Best Local Similarity   100.0%; Pred. No. 0.0001;		
	Matches     18; Conservative       0; Mismatches     0; Indels     0; Gaps     0;		
OY	1 RLLRAVIMGAPSGSKGT V 18		
Dd	6 RLRLAIVMGAPSGSKGT V 23		
	RESULT 6		
	AAB93066		
XX	ID AAB93066 standard: Protein; 227 AA.		
XX			
XX	AAB93066;		
DT			
XX	26-JUN-2001 (first entry)		
DE			
XX	Human protein sequence SEQ ID NO:11883.		
XX			
KW	Human; primer: detection; diagnosis; antisense therapy; gene therapy.		
OS	Homo sapiens.		
XX			
PX	EPI074617-A2.		
PD			
XX	07-FEB-2001.		
PF			
XX	28-JUL-2000; 2000EP-0116126.		
PR			
XX	29-JUL-1999; 99JP-0248036.		
PR	27-AUG-1999; 99JP-0300253.		
PR	11-OAN-2000; 2000JP-0118776.		
PR	02-MAY-2000; 2000JP-0183767.		
PR	09-JUN-2000; 2000JP-0241899.		
PA			
XX	(HELI-) HELIX RES INST.		
XX			
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
DR			
XX	WPI: 2001-318749/34.		
PT			
PT	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		

XX PS Claim 8; SEQ ID 11883; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 88; DB 22; Length 227;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGKGTV 18

Db 6 RLRAVIMGAPSGKGTV 23

# RESULT 7

ID AAB93487 standard; Protein; 227 AA.

XX AAB93487;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:12786.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

PN EP1074617-A2.

XX 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

PT primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

XX PS Claim 8; SEQ ID 12786; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 88; DB 22; Length 227;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGKGTV 18

Db 6 RLRAVIMGAPSGKGTV 23

# RESULT 8

ID AAB85885 standard; Protein; 227 AA.

XX AAB85885;

DT 30-NOV-2001 (first entry)

DE Human adenylate kinase 3 (AK3)-like protein.

XX Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;

KW MELAS; central nervous system disorder; epilepsy; skeletal muscle;

KW muscle disease; electron transfer disorder; Leber disease; human;

KW diabetes mellitus; Pearson disease; Parkinson's disease.

XX Homo sapiens.

PN WO200109346-A1.

XX 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05066.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;

PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;

XX Nishikawa T, Kimura K;

DR WPI: 2001-564737/63.  
 DR N-PSDB: AAA47197.  
 XX  
 PT New gene encoding an adenylate kinase 3-like protein, and the protein  
 PT and antibodies to it, useful for diagnosis of brain disease e.g.  
 PT epilepsy, muscle disease, genetic disorder, diabetes  
 XX  
 PS Claim 1; Page 34-35; 41pp; Japanese.  
 XX  
 CC The invention relates to a cDNA (clone C-WT28P2000329) encoding a novel  
 CC adenylate kinase 3 (AK3)-like protein. C-WT28P2000329 has functions of  
 CC converting extracellular signals into intracellular signals and changing  
 CC cell morphology. The AK3-like protein, polynucleotides and antibodies are  
 CC useful in the investigation of diseases such as MEAS (cerebral accident  
 CC condition with hyperlactacidemia), central nervous system disorder.  
 CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer  
 CC disorders, liver disease, diabetes mellitus, Pearson disease, Parkinson's  
 CC disease, metabolism disorders. They are useful for developing diagnostics  
 CC and treatment agents. The present sequence represents the human AK3-like  
 CC protein of the invention.  
 CC  
 SO Sequence 227 AA:  
 Query Match 100.0%; Score 88; DB 22; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLRAVIMGAPSGSGKTV 18  
 DB 6 RLRAVIMGAPSGSGKTV 23  
 RESULT 9  
 ID ABB12326 standard; peptide: 239 AA.  
 AC ABB12326;  
 XX  
 DT 11-JAN-2002 (first entry)  
 XX  
 DE Human secreted protein homologue, SEQ ID NO:2696.  
 XX  
 CC Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 CC haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 CC inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 CC proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 CC myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 CC chronic inflammatory condition; proliferative retinopathy;  
 CC atherosclerosis; coronary heart disease; arterial ischaemia;  
 CC bone disorder; osteoporosis; vascular growth disorder;  
 CC tissue regeneration; wound healing; infection; immune disorder;  
 CC cell culture; drug screening; gene therapy; antiinflammatory;  
 CC antiasthmatic; antiarthritis; haemostatic; antiatherosclerotic;  
 CC cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;  
 CC antifungal; vulnery; antiulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157188-A2.  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001MO-US03800.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI: 2001-457740/49.  
 DR N-PSDB: ABA09570.

XX  
 CC Human proteins and DNA encoding sequences useful for preventing,  
 CC treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 XX  
 PS Claim 20; Page 333; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g. of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.  
 CC  
 SO Sequence 239 AA:  
 Query Match 100.0%; Score 88; DB 22; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLRAVIMGAPSGSGKTV 18  
 DB 18 RLRAVIMGAPSGSGKTV 35  
 RESULT 10  
 ID AAM40685 standard; protein: 239 AA.  
 AC AAM40685;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 5616.  
 XX  
 CC Human; neutrophic; immunosuppressant; cytostatic; gene therapy; cancer;  
 CC peripheral nervous system; neuropathy; central nervous system; CNS;  
 CC Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 CC amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 CC chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 CC leukaemia.  
 XX

OS Homo sapiens.  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0538042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HXSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI: 2001-442253/47.  
 DR N-PSDB: AA159841.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 2; SEQ ID NO 5616; 10078bp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA38642-AA42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 CC  
 XX  
 SQ Sequence 239 AA;  
 Query Match 100.0%; Score 88; DB 22; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLLRAVINGAPGSGKGT 18  
 DB 18 RLLRAVINGAPGSGKGT 35  
 RESULT 11  
 AAG73865  
 ID AAG73865 standard; Protein: 256 AA.  
 XX  
 AC AAG73865;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human colon cancer antigen protein SEQ ID NO:4629.  
 XX  
 KW Human: colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma.  
 XX  
 OS Homo sapiens.

XX  
 PN WO200122920-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000WO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PI WPI: 2001-235357/24.  
 DR N-PSDB: AAH33296.  
 XX  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 11; Page 6430-6431; 9803pp; English.  
 XX  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated P,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAH77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 CC  
 XX  
 SQ Sequence 256 AA;  
 Query Match 100.0%; Score 88; DB 22; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RLLRAVINGAPGSGKGT 18  
 DB 35 RLLRAVINGAPGSGKGT 52  
 RESULT 12  
 AAB12441  
 ID AAB12441 standard; Protein: 227 AA.  
 XX  
 AC AAB12441;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE AK3 protein sequence.  
 XX  
 KW Human: mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.  
 KW Unidentified.  
 XX  
 PN CN1249340-A.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 28-SEP-1998; 98CN-0119439.  
 XX

PR	28-SEP-1998;	98CN-0119439.
PA	(XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.	
PB		
PI	Yu L, Zhao Y, Bi A;	
PL		
PM	WPI: 2000-400718/35.	
PN	N-Psdb; AAA60585.	
PO		
PP	Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,	
PQ	its encode sequence -	
PS	Example 2; Fig 2; 20pp; Chinese.	
PT		
PV		
PW	The present invention describes a new ribotide sequence of human gene,	
PX	that is, the cDNA sequence of human mitochondrial matrix GTP:AMP	
PY	phosphotransferase (GTP3P) and the encoded polypeptide. The present	
PZ	sequence represents the AK3 protein sequence which is used in	
QA	comparison with human GTP3P in the present invention.	
QB		
QC	Sequence 227 AA;	
QD		
QE	Query Match	95.5%; Score 84; DB 21; Length 227;
QF	Best Local Similarity	94.4%; Fred. NO. 0.00037;
QG	Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0.
QH		
QI	1 RLLRAVIMGAPSGKGT V 18	
QJ	6 RLLRAAIMGAPSGKGT V 23	
QK		
QL	RESULT 13	
QM	AAE11778	
QN	ID AAE11778 standard; Protein; 224 AA.	
QO	XX AC AAE11778;	
QP	XX DT 18-DEC-2001 (first entry)	
QQ	XX DE Human kinase (PKIN)-12 protein.	
QR	XX KW Human kinase; PKIN: gene therapy; adenocarcinoma; immune disorder; gout;	
QS	KW Cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome;	
QT	KW AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;	
QU	KW atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;	
QV	KW myasthenia gravis; cirrhosis; cataract; growth and development disorder;	
QW	KW seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;	
QX	KW lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease;	
QY	KW obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular;	
QZ	antimicrobial; cytostatic; antiinflammatory; asthma.	
R0	XX OS Homo sapiens.	
R1	XX XX	
R2	Key Location/Qualifiers	
R3	FT Region 1..126	
R4	/note= "Adenylate kinase"	
R5	FT Region 8..23	
R6	/note= "Shikimate kinase family"	
R7	FT Region 9..25	
R8	/note= "Adenylate kinase"	
R9	FT Region 10..190	
R10	/note= "Adenylate kinase"	
R11	FT Region 33..76	
R12	/note= "Adenylate kinase"	
R13	FT Region 80..94	
R14	/note= "Adenylate kinase"	
R15	FT Domain 85..96	
R16	/note= "Adenylate kinase motif"	
R17	FT Region 107..124	
R18	/note= "Shikimate kinase family"	
R19	FT Region 132..162	
R20	/note= "Adenylate kinase"	
R21	FT Region	
R22	XX XX	

PM	WO200181555-A2.
PD	
XX	01-NOV-2001.
PF	20-APR-2001; 2001WO-US12992.
XX	
PR	20-APR-2000; 2000US-199021P.
PR	28-APR-2000; 2000US-200226P.
PR	05-MAY-2000; 2000US-202339P.
PR	11-MAY-2000; 2000US-202305P.
PR	18-MAY-2000; 2000US-205564P.
PR	26-MAY-2000; 2000US-207739P.
PR	01-JUN-2000; 2000US-208795P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
PI	Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
PI	Bandman O, Lu DM, Lal P, Burford N, Khn FA, Walla NK, Yao MG;
PI	Patterson C, Burrill JD, Marcus GA, Zingler KA, Reipon SA, Lu Y;
PI	Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
PI	Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
PI	Gururajan R;
XX	
DR	WPI: 2001-611740/70.
DR	N-PSDB: AADI6827.
PT	Human kinases and nucleic acids, useful for preventing diagnosing and
PT	treating cancers, inflammation and immune disorders -
XX	
PS	Claim 1, Page 138-139; 166pp; English.
XX	
XX	The present invention relates to human kinases (PKIN) and the nucleic
CC	acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is
CC	used in the prevention, diagnosis and treatment of diseases cancers,
CC	adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease,
CC	acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies,
CC	gout, microbial infections, cardiovascular disease and/or inflammation;
CC	myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial
CC	infarction, cataract, growth and development disorder, seizure disorder,
CC	pulmonary emphysema, Gaucher's disease, lipid disorder, lipid storage
CC	disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
CC	PKIN may be used to treat disorders associated with decreased PKIN
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of PKIN by expressing inactive proteins or to
CC	supplement the patient's own production of PKIN. PKIN nucleic acids may be
CC	used to produce the PKIN polypeptide, by inserting the nucleic acids into
CC	a host cell and culturing the cell to express the protein. PKIN nucleic
CC	acid and its complementary sequences may also be used as DNA probes in
CC	diagnostic assays to detect and quantitate the presence of similar
CC	nucleic acid sequences in samples and therefore which patients may be
CC	in need of restorative therapy. The present sequence is human PKIN-12
CC	protein.
XX	
SO	Sequence 224 AA:
OY	1 RLLRAVINGAPGSGKGTV 18
DB	4 KLLRAVILGPPGSGKGTV 21
XX	
XX	RESULT 14
XX	ABB62530
ID	ABB62530 standard; Protein: 216 AA.
XX	ABB62530;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 14362.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL06633.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS Disclosure; SEQ ID NO 14382; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB101840-AB161175) and the encoded DNA  
 CC sequences (AB101840-AB161175) and the encoded proteins  
 CC (AB101840-AB161175).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 216 AA;  
 Query Match 84.1%; Score 74; DB 22; Length 216;  
 Best Local Similarity 72.2%; Pred. No. 0.0088;  
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 RLRAVINGAPGSGKGTV 18  
 Db 4 KIRRAVIGAPGSGKGTI 21  
 RESULT 15  
 AAB53619  
 ID AAB53619 standard; Protein; 214 AA.  
 XX  
 AC AAB53619;  
 XX  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Human colon cancer antigen protein sequence SEQ ID NO:1159.  
 XX  
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;  
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; renal disorder;  
 KW infectious disease; cardiovascular disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055351-A1.  
 XX

PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05883.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587534/55.  
 DR N-PSDB; AAC98376.  
 XX  
 PT Colon cancer associated gene sequences, referred to as colon cancer  
 PT antigens, useful for the treatment, prevention, and diagnosis of colon  
 PT disorders such as colon cancer -  
 XX  
 XX  
 PS Claim 11: Page 1741-1742; 2104pp; English.  
 XX  
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The  
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;  
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and  
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,  
 CC proteins and antibodies to the proteins are useful for the prevention,  
 CC treatment and diagnosis of colon disorders, such as colon cancer. The  
 CC polynucleotides may be used in diagnostics and research, such as for  
 CC chromosome identification, and as hybridisation probes. The proteins  
 CC may also be used to prevent diseases such as neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, wounds, renal disorders, infectious  
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
 CC AAB54007 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 214 AA;  
 Query Match 79.5%; Score 70; DB 21; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 AVINGAPGSGKGTV 18  
 Db 1 AVINGAPGSGKGTI 14  
 Search completed: April 24, 2003, 10:19:29  
 Job time : 37 secs





GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 ; Search time 29 Seconds  
(without alignments)  
127.891 Million cell updates/sec

Title: US-10-006-190-1\_COPY\_6\_23  
Perfect score: 88  
Sequence: 1 RLRAVINGAGSGKGV 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp-archaea:\*
- 2: sp-bacteria:\*
- 3: sp-fungi:\*
- 4: sp-human:\*
- 5: sp-invertebrate:\*
- 6: sp-mammal:\*
- 7: sp-mhc:\*
- 8: sp-organelle:\*
- 9: sp-phage:\*
- 10: sp-plant:\*
- 11: sp-rodent:\*
- 12: sp-virus:\*
- 13: sp-vertebrate:\*
- 14: sp-unclassified:\*
- 15: sp-virus:\*
- 16: sp-bacteriophage:\*
- 17: sp-archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	189	11 Q9D8W6	Q9D8W6 mus musculus
2	88	100.0	227	4 Q9NPB4	Q9NPB4 h cDNA flj1
3	88	100.0	227	6 Q95J94	Q95J94 oryctolagus
4	88	100.0	227	11 Q9D8W5	Q9D8W5 mus musculus
5	88	100.0	227	11 Q9D8W5	Q9D8W5 mus musculus
6	88	100.0	227	11 Q9D7Z1	Q9D7Z1 mus musculus
7	88	100.0	227	11 Q9D7Z1	Q9D7Z1 mus musculus
8	74	84.1	216	5 Q9VG06	Q9VG06 drosophila
9	65	73.9	231	3 Q93985	Q93985 neocallimys
10	65	73.9	231	3 Q93987	Q93987 pteromyces s
11	64	72.7	232	3 Q93986	Q93986 neocallimys
12	62	70.5	55	2 Q9XDI6	Q9XDI6 bacteroides
13	60	68.2	202	4 Q9KWA2	Q9KWA2 agrobacteri
14	60	68.2	232	11 Q9CY37	Q9CY37 homo sapien
15	58	65.9	130	11 Q8R4A6	Q8R4A6 mus musculus
16	58	65.9	248	11 Q9ESC4	Q9ESC4 mus musculus

17	58	65.9	331	11 Q9ESC5	Q9ESC5 mus musculus
18	58	65.9	437	4 Q96RC0	Q96RC0 homo sapien
19	58	65.9	437	4 Q8WUY4	Q8WUY4 homo sapien
20	58	65.9	437	11 Q9CZU4	Q9CZU4 mus musculus
21	58	65.9	437	11 Q9Z5U1	Q9Z5U1 mus musculus
22	58	65.9	444	4 Q96LE2	Q96LE2 homo sapien
23	57	64.8	237	5 Q9W1D0	Q9W1D0 drosophila
24	57	64.8	240	5 Q9U915	Q9U915 drosophila
25	56	63.6	221	16 Q8R7X4	Q8R7X4 thermococcus
26	55	62.5	211	16 Q8RE31	Q8RE31 fusobacteri
27	55	62.5	220	5 Q9Y0A8	Q9Y0A8 cryptospori
28	55	62.5	229	5 Q964H2	Q964H2 plasmodium
29	54	61.4	222	5 Q8R5S3	Q8R5S3 trypanosoma
30	53	60.2	177	16 Q97G88	Q97G88 clostridium
31	53	60.2	248	10 Q9FK35	Q9FK35 arabidopsis
32	53	60.2	588	10 Q8VY11	Q8VY11 arabidopsis
33	52	59.1	191	5 Q20230	Q20230 caenorhabd
34	52	59.1	191	5 Q17622	Q17622 caenorhabd
35	52	59.1	193	11 Q920P5	Q920P5 mus musculus
36	52	59.1	196	16 Q8UE38	Q8UE38 agrobacteri
37	52	59.1	216	1 Q9P9D2	Q9P9D2 uncultured
38	52	59.1	262	16 Q9WZM6	Q9WZM6 thermotoga
39	52	59.1	283	10 Q9F1J7	Q9F1J7 arabidopsis
40	51	58.0	208	5 Q00846	Q00846 parametium
41	51	58.0	211	5 Q9U1D3	Q9U1D3 leishmania
42	51	58.0	510	12 Q65723	Q65723 barley str1
43	51	58.0	512	12 Q65718	Q65718 barley str1
44	51	58.0	512	12 Q65722	Q65722 barley str1
45	51	58.0	512	12 Q65725	Q65725 barley str1

#### ALIGNMENTS

#### RESULT 1

Q9D8W6

PRELIMINARY:

PRT:

189 AA.

Q9D8W6: 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE 10 day old male pancreas cDNA, RIKEN full-length enriched library,  
clone:1810027K10, full insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavola H.,  
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochila H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barish G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.D., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.,  
RT \*Functional annotation of a full-length mouse cDNA collection.\*;  
CC Nature 409:685-690(2001).  
DR EMBL: AK007618; BAB25139.1; -.

DR HSSP: P08760; 2AK3.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR InterPro: IPR000623; Shik\_kinase.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR PRINTS: PR01100; SHIKIMTKINASE.  
 DR PRODOM: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 189 AA; 21193 MW; 822ADB21804F5336 CRC64;

Query Match 100.0%; Score 88; DB 11; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKTV 18  
 |||  
 DB 6 RLRAVIMGAPSGSGKTV 23

RESULT 2

ID Q9NPB4 PRELIMINARY; PRT: 227 AA.

AC Q9NPB4;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE CNA FLJ11089 fis, clone PLACE105305, highly similar to GRP:AMP  
 DE phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 fis,  
 DE clone NTREP300359, highly similar to GRP:AMP phosphotransferase  
 DE mitochondrial) (CDNA FLJ14628 fis, clone NTREP2000329, highly similar  
 DE to GRP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa  
 DE protein).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PLACENTA;  
 RA Iisogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,  
 RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
 RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;  
 RT "NEDO human cDNA sequencing project."  
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Iisogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,  
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,  
 RA Masuho Y., Kanehori K.;  
 RT "NEDO human cDNA sequencing project."  
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Iisogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,  
 RA Magatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
 RA Niromiya K., Iwayanagi T.;  
 RT "NEDO human cDNA sequencing project."  
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LYMPH;  
 RA Strausberg R.;  
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL: AK001951; BAA91996.1;

DR EMBL: AK001553; BAA91753.1;  
 DR EMBL: AK027534; BAB55183.1;  
 DR EMBL: BC013771; AAH13771.1;  
 DR HSSP: P08760; 2AK3.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR InterPro: IPR000623; Shik\_kinase.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR PRINTS: PR01100; SHIKIMTKINASE.  
 DR PRODOM: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW Hypothetical protein; Kinase; Transferase.  
 SQ SEQUENCE 227 AA; 25565 MW; 98ADEFAFD9C9CEFCRC64;

Query Match 100.0%; Score 88; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKTV 18  
 |||  
 DB 6 RLRAVIMGAPSGSGKTV 23

RESULT 3

ID Q95J94 PRELIMINARY; PRT: 227 AA.

AC Q95J94;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Adenylate kinase 3.  
 DE Oryctolagus cuniculus (Rabbit).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-RENAL PROXIMAL TUBULE;  
 RX MEDLINE-21240235; PubMed-11342145;  
 RA Brochiero E., Coady M.J., Klein H., Laprade R., Lapointe J.Y.;  
 RT "Activation of an ATP-dependent K(+) conductance in Xenopus oocytes by  
 RT expression of adenylate kinase cloned from renal proximal tubules."  
 RL Biochim. Biophys. Acta 1510:29-42(2001).  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL: AF417508; AL07503.1;  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRODOM: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; UNKNOWN\_1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 227 AA; 25610 MW; ECDIDDF89228A4E CRC64;

Query Match 100.0%; Score 88; DB 6; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLRAVIMGAPSGSGKTV 18  
 |||  
 DB 6 RLRAVIMGAPSGSGKTV 23

RESULT 4

ID Q9DBM5 PRELIMINARY; PRT: 227 AA.

AC Q9DBM5;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Adenylate kinase 3 alpha like.  
 GN AKL3L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Noridone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK004864; BAB23625.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660FDF1E991DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLLRAVINGAPSGKGTV 18
DB 6 RLLRAVINGAPSGKGTV 23
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK005194; BAB23876.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLLRAVINGAPSGKGTV 18
DB 6 RLLRAVINGAPSGKGTV 23
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RESULT 5
O9DB57 PRELIMINARY: PRT: 227 AA.
AC O9DB57;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Adenylate kinase 3 alpha like.
GN AKL3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Noridone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK004864; BAB23625.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660FDF1E991DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLLRAVINGAPSGKGTV 18
DB 6 RLLRAVINGAPSGKGTV 23
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RESULT 6
O9DB721 PRELIMINARY: PRT: 227 AA.
AC O9DB721;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Adenylate kinase 3 alpha like.
GN AKL3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK005194; BAB23876.1; -.
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RLLRAVINGAPSGKGTV 18
DB 6 RLLRAVINGAPSGKGTV 23
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RP SEQUENCE FROM N.A.  
 RC TISSUE-COLON;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL: AK008681; BAB25829.1; -  
 DR EMBL: BC016432; AAH16432.1; -  
 DR EMBL: BC019174; AAH19174.1; -  
 DR EMBL: BC024871; AAH24871.1; -  
 DR HSSP: P08760; 2AK3.  
 DR MGD: MG11860835; AK131.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR PRINTS: PR01100; SHIKMTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 DR Kinase: Transferase.  
 SQ SEQUENCE 227 AA; 25426 MW; 6601DF10971DE5AC CRC64;

Query Match 100.0%; Score 88; DB 11; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 7; Se-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLRAVIMGAPGSGKTV 18  
 Db 6 RLRAVIMGAPGSGKTV 23

RESULT 7  
 Q9VGU6 PRELIMINARY; PRT; 216 AA.  
 AC Q9VGU6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE CG6612 protein (Adenylate kinase isozyme 3).  
 GN ADK3 OR DAK3 OR CG6612.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferris S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Noma T.;  
 RT "DAK3.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL: AE003689; AAF54578.1; -  
 DR EMBL: AB050622; BAB4152.1; -  
 DR HSSP: P08760; 2AK3.  
 DR FlyBase: FBgn0042094; Adk3.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.  
 DR PRINTS: PR00094; ADENYLTKINASE.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 DR Kinase: Transferase.  
 SQ SEQUENCE 216 AA; 24145 MW; 6AB49A756D23091B CRC64;

Query Match 84.1%; Score 74; DB 5; Length 216;  
 Best Local Similarity 72.2%; Pred. No. 0 0068;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLRAVIMGAPGSGKTV 18  
 Db 4 KIFRAVIMGAPGSGKTV 21

RESULT 8  
 Q93985 PRELIMINARY; PRT; 231 AA.  
 AC Q93985;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Adenylate kinase (EC 2.7.4.3) (Fragment).  
 GN HDGAKL2.1.  
 OS Neocallimastix frontalis (Rumen fungus).  
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;  
 OC Neocallimastixaceae; Neocallimastix.  
 OX NCBI\_TaxID=4757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-L2;  
 RA Voncken F., Boyma B., Verhagen E., van Wesel R., van der Drift C.,  
 RA Veenhuis M., Hackstein J., Vogels G.;  
 RT Evidence for a chimeric origin of chytrid hydropodomes.";  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 DR EMBL: AJ274658; CAA12055.1; -  
 DR HSSP: P07170; 1AKY.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase; 1.

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DR PRINTS: PR00094: ADENYLTKINASE.
DR PRODOM: PD000657: Adenylate_kin. 1.
DR PROSITE: PS00113: ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 231
SQ SEQUENCE 231 AA; 25353 MW; 844B51EB554676A2 CRC64;

Query Match
Best Local Similarity 73.9%; Score 65; DB 3; Length 231;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 9
OY 093987 PRELIMINARY; PRT; 231 AA.
AC 093987;
DT 01-MAY-1999 (TREMBLrel. 10, Created).
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (Fragment).
GN HDGAK2.
OS Pteromyces sp. E2.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Pteromyces.
ON NCBI_TaxID=73868;
RX [1]
RP SEQUENCE FROM N.A.
RA Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,
RA Veenhuis M., Hackstein J., Vogels G.;
RT "Evidence for a chimeric origin of chytrid hydrogenosomes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AJ224660; CAI12057.1; -.
DR HSSP: P07170; 1AKY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 231
SQ SEQUENCE 231 AA; 25407 MW; 64279A95550570BF CRC64;

Query Match
Best Local Similarity 73.9%; Score 65; DB 3; Length 231;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 10
OY 093986 PRELIMINARY; PRT; 232 AA.
AC 093986;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (Fragment).
GN HDGAK12.2.
OS Neocallimastix frontalis (Rumen fungus).
OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
OC Neocallimastixaceae; Neocallimastix.
ON NCBI_TaxID=4757;
RX [1]
RP SEQUENCE FROM N.A.
RA Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,

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RA Veenhuis M., Hackstein J., Vogels G.;
RT "Evidence for a chimeric origin of chytrid hydrogenosomes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AJ224659; CAI12056.1; -.
DR HSSP: P07170; 1AKY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; transferase.
FT NON_TER 232
SQ SEQUENCE 232 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;

Query Match
Best Local Similarity 72.7%; Score 64; DB 3; Length 232;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LRAVINGAPSGSGKT 17
Db 10 LRMVIMGPSPSGKT 24

RESULT 11
OY 09XD16 PRELIMINARY; PRT; 55 AA.
AC 09XD16;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
DE (Fragment).
GN ADK.
OS Bacteroides fragilis.
OC Bacteria; CFP group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
OC Bacteroides.
ON NCBI_TaxID=817;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN-NCTC 9343;
RX MEDLINE=99307214; PubMed=10377135;
RA Constock L.E., Coyne M.J., Tzlanabos A.O., Pantosti A.,
RA Onderdonk A.B., Kasper D.L.;
RT "Analysis of a capsular polysaccharide biosynthesis locus of
RT Bacteroides fragilis.";
RL Infect. Immun. 67:3525-3532(1999).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DR EMBL: AF048749; AAD40729.1; -.
DR HSSP: P27142; 12IN.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin; 1.
KW ATP-binding; Kinase; transferase.
FT NON_TER 55
SQ SEQUENCE 55 AA; 5849 MW; 027DCA433E12908A CRC64;

Query Match
Best Local Similarity 70.5%; Score 62; DB 2; Length 55;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 LRAVINGAPSGSGKT 17
Db 1 LRAVINGAPSGSGKT 16

RESULT 12

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OY	3	LRAVINGAPGSGKGT	17
		: : :     -	
D6	1	MRLIMGPBGSGKGT	15
 RESULT 13			
ID	08TCY3	PRELIMINARY;	PRT: 202 AA.
AC	08TCY3:		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DE	Adeynylate kinase 2 variant AKZC.		
GN	AKZ.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Guo J.;		
RL	"Novel Isoforms of Human Adeynylate Kinase 2."		
DR	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
KW	EMBL; AY080899; AAL87027.1; ..		
SQ	kinase.		
	SEQUENCE 202 AA; 2265 MW; AE7593A8ADBDD0CF CRC64;		
 Query Match 68.2%; Score 60; DB 4; Length 202; Best Local Similarity 66.7%; Pred. NO. 0.6; Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0.			
OY	3	LRAVINGAPGSGKGT	17
		: : :	
D6	16	IHAVLLGGPGAGKT	30
 RESULT 14			
ID	09CY37	PRELIMINARY;	PRT: 232 AA.
AC	09CY37:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Adeynylate kinase 2.		
GN	AKZ.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Fukuda S.,		
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Mikaldo I., Pesole G., Quackenbush J.,		
RA	Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blahe J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzairelli J., Momberts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,		
RA	Wysshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
TL	Nature 409:685-690(2001).		

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RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK010951; BAB27286.1; -
DR EMBL: BC008610; AA08610.1; -
DR HSSP: P08166; IAK2.
DR MGD: MGI:87978; AK2.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PRO0094; ADENYLTKINASE.
DR PRODOM: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW kinase; transferase.
SQ SEQUENCE 232 AA; 25605 MW; EDD60400562323CF CRC64;

Query Match
Best Local Similarity 68.2%; Score 60; DB 11; Length 232;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVINGAPGSGKGT 17
   :|||:|||||
Db 16 IRAVLLGPGAGKGT 30

RESULT 15
Q8R4A6
ID Q8R4A6 PRELIMINARY; PRT; 130 AA.
AC Q8R4A6;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ERA-like protein 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Ji Z., Chen S., Liu J., Zhao Z., Chai Y., Liu X., Chen N.;
RT "Mouse chromosome 11."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF486635; AAM08321.1; -.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 13805 MW; 38B0749DAE63C5BB CRC64;

Query Match
Best Local Similarity 65.9%; Score 58; DB 11; Length 130;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLRAVINGAPGSGKGT 18
   |::|::|::|::|
Db 78 RVLRLVLLGAPNCKSTL 95

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Search completed: April 24, 2003, 10:18:17  
 Job time : 32 secs

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